10/579393 10 15 MAY 2006 PCT/FI2004/000679

SEQUENCE LISTING

1/13

<110> Nordlund, Henri Rainer et al.

<120> Avidin mutants

<130> BP110588

<160> 29

<170> PatentIn version 3.1

<210> 1

<211> 152 <212> PRT <213> Gallus gallus

<400> 1

Met Val His Ala Thr Ser Pro Leu Leu Leu Leu Leu Leu Ser Leu 10

Ala Leu Val Ala Pro Gly Leu Ser Ala Arg Lys Cys Ser Leu Thr Gly

Lys Trp Thr Asn Asp Leu Gly Ser Asn Met Thr Ile Gly Ala Val Asn

Ser Arg Gly Glu Phe Thr Gly Thr Tyr Ile Thr Ala Val Thr Ala Thr 55

Ser Asn Glu Ile Lys Glu Ser Pro Leu His Gly Thr Gln Asn Thr Ile 65

Asn Lys Arg Thr Gln Pro Thr Phe Gly Phe Thr Val Asn Trp Lys Phe 90

Ser Glu Ser Thr Thr Val Phe Thr Gly Gln Cys Phe Ile Asp Arg Asn 105

. Gly Lys Glu Val Leu Lys Thr Met Trp Leu Leu Arg Ser Ser Val Asn 115 120

Asp Ile Gly Asp Asp Trp Lys Ala Thr Arg Val Gly Ile Asn Ile Phe

Thr Arg Leu Arg Thr Gln Lys Glu 150

<210> 2 <211> 298 <212> PRT

<213> Gallus gallus

<400> 2

Met Val His Ala Thr Ser Pro Leu Leu Leu Leu Leu Leu Leu Ser Leu 1 5 10 15

Ala Leu Val Ala Pro Gly Leu Ser Ala Arg Lys Arg Thr Gln Pro Thr 20 25 30

Phe Gly Phe Thr Val Asn Trp Lys Phe Ser Glu Ser Thr Thr Val Phe 35 40 45

Thr Gly Gln Cys Phe Ile Asp Arg Asn Gly Lys Glu Val Leu Lys Thr 50 55 60

Met Trp Leu Leu Arg Ser Ser Val Asn Asp Ile Gly Asp Asp Trp Lys 65 70 75 80

Ala Thr Arg Val Gly Ile Asn Ile Phe Thr Arg Leu Arg Thr Gln Lys 85 90 95

Glu Gly Gly Ser Gly Gly Ser Ala Arg Lys Cys Ser Leu Thr Gly Lys 100 105 110

Trp Thr Asn Asp Leu Gly Ser Asn Met Thr Ile Gly Ala Val Asn Ser 115 120 125

Arg Gly Glu Phe Thr Gly Thr Tyr Ile Thr Ala Val Thr Ala Thr Ser 130 135 140

Asn Glu Ile Lys Glu Ser Pro Leu His Gly Thr Gln Asn Thr Ile Asn 145 150 155 160

Lys Ser Gly Gly Ser Thr Thr Val Phe Thr Gly Gln Cys Phe Ile Asp 165 170 175

Arg Asn Gly Lys Glu Val Leu Lys Thr Met Trp Leu Leu Arg Ser Ser 180 185 190

Val Asn Asp Ile Gly Asp Asp Trp Lys Ala Thr Arg Val Gly Ile Asn 195 200 205

Ile Phe Thr Arg Leu Arg Thr Gln Lys Glu Gly Gly Ser Gly Gly Ser 210 220

Ala Arg Lys Cys Ser Leu Thr Gly Lys Trp Thr Asn Asp Leu Gly Ser 230 225

Asn Met Thr Ile Gly Ala Val Asn Ser Arg Gly Glu Phe Thr Gly Thr 250

Tyr Ile Thr Ala Val Thr Ala Thr Ser Asn Glu Ile Lys Glu Ser Pro

Leu His Gly Thr Gln Asn Thr Ile Asn Lys Arg Thr Gln Pro Thr Phe

Gly Phe Thr Val Asn Trp Lys Phe Ser Glu 290 295

<210> 3

<211> 6 <212> PRT <213> Artificial sequence <223> linker

<400> 3

Gly Gly Ser Gly Gly Ser

<210> 4

<211> 31

<212> DNA

<213> Artificial sequence

<223> primer

<400> 4

ctgctagatc tatggtgcac gcaacctccc c

31

<210> 5

<211> 19 <212> DNA <213> Artificial sequence <223> primer

<400> 5

cctggcagag aggccggga

19

<210> 6

<211> 20

<212> DNA

<213> Artificial sequence

<223> primer

<400> 6

aagaggaccc agcccacctt

20

	DNA Artificial sequence	
<223>	primer	
<400>		
ggagco	teeg gageeteect cettetgtgt gegeag	36
<210>		
<211> <212>		
	Artificial sequence	
	primer	
-400-		
<400>	tccg gaggeteege cagaaagtge tegetg	36
55-55-		
<210>	0	
<211>		
<212>		
<213>	Artificial sequence	
<223>	primer	
<400>	9	
	agct tcacttgttg atggtgtttt g	31
<210>	10	
<211>	21	
<212>		
	Artificial sequence	
<223>	primer	
<400>	10	
aagtc	cacca ctgtcttcac g	21
<210>		
<211>		
<212>		
	Artificial sequence	
<223>	primer	
<400>		32
agaca	aagct tcactctgaa aacttccaat tg	34
<210>		
<211>		
<212>		
<213>		
<423>	primer	
<400>		
gtggt	ggatc cgccggactt gttgatggtg ttttgtgt	38

WO 2005/047317

ggcggatcta ccactgtc

<210> 19

PCT/FI2004/000679

<400>			
gacagt	ggta gatccgcc	18	
<210>	20 .		
<211>	29 .		
<212>	DNA Artificial sequence		
	primer		
<400>			
ccggca	gatc taccactgtc ttcacgggc	29	
	•		
<210>			
<211> <212>			
	Artificial sequence		
	primer		
<400>			
atcctc	ggat cccgatccgg aacctccctc tgaaaacttc	40	
<210>			
<211>			
<212>	DNA Artificial sequence		
	primer		
<400>	22		
	ggtg getggateeg getetggeag eggeaggaee eageee	46	
<210>	23		
<211>			
<212>			
	Artificial sequence primer		
\223 /	primer		
<400>			
ctacaa	atgt ggtatggctg	20	
<210>.			
<211> <212>			
<213>			
<400>	24		
Met Va 1	l His Ala Thr Ser Pro Leu Leu Leu Leu Leu Leu Sér Leu 5 10 15		

Ala Leu Val Ala Pro Gly Leu Ser Ala Arg Lys Arg Thr Gln Pro Thr

20 25 30

Phe Gly Phe Thr Val Asn Trp Lys Phe Ser Glu Ser Thr Thr Val Phe 35 40 45

Thr Gly Gln Cys Phe Ile Asp Arg Asn Gly Lys Glu Val Leu Lys Thr 50 55 60

Met Trp Leu Leu Arg Ser Ser Val Asn Asp Ile Gly Asp Asp Trp Lys 65 70 75 80

Ala Thr Arg Val Gly Ile Asn Ile Phe Thr Arg Leu Arg Thr Gln Lys 85 90 95

Glu Gly Gly Ser Gly Gly Ser Ala Arg Lys Cys Ser Leu Thr Gly Lys
100 105 110

Trp Thr Asn Asp Leu Gly Ser Asn Met Thr Ile Gly Ala Val Asn Ser 115 120 125

Arg Gly Glu Phe Thr Gly Thr Tyr Ile Thr Ala Val Thr Ala Thr Ser 130 135 140

Asn Glu Ile Lys Glu Ser Pro Leu His Gly Thr Gln Asn Thr Ile Asn 145 150 155 160

Lys Ser Gly Gly Ser Thr Thr Val Phe Thr Gly Gln Cys Phe Ile Asp 165 170 175

Arg Asn Gly Lys Glu Val Leu Lys Thr Met Trp Leu Leu Arg Ser Ser 180 185 190

Val Asn Asp Ile Gly Asp Asp Trp Lys Ala Thr Arg Val Gly Ile Asn 195 200 205

Ile Phe Thr Arg Leu Arg Thr Gln Lys Glu Gly Gly Ser Gly Gly Ser 210 220

Ala Arg Lys Cys Ser Leu Thr Gly Lys Trp Thr Asn Asp Leu Gly Ser 225 230 235 240

Asn Met Thr Ile Gly Ala Val Asn Ser Arg Gly Glu Phe Thr Gly Thr 245 250 255

Tyr Ile Thr Ala Val Thr Ala Thr Ser Asn Glu Ile Lys Glu Ser Pro 260 265 270 Leu His Gly Thr Gln Asn Thr Ile Asn Lys Arg Thr Gln Pro Thr Phe 275 280 285

Gly Phe Thr Val Asn Trp Lys Phe Ser Glu Gly Gly Ser Gly Ser Gly 290 295 300

Ser Gly Ser Gly Ser Gly Arg Thr Gln Pro Thr Phe Gly Phe Thr Val 305 310 315 320

Asn Trp Lys Phe Ser Glu Ser Thr Thr Val Phe Thr Gly Gln Cys Phe 325 330 335

Ile Asp Arg Asn Gly Lys Glu Val Leu Lys Thr Met Trp Leu Leu Arg 340 345 350

Ser Ser Val Asn Asp Ile Gly Asp Asp Trp Lys Ala Thr Arg Val Gly 355 360 365

Ile Asn Ile Phe Thr Arg Leu Arg Thr Gln Lys Glu Gly Gly Ser Gly 370 375 380

Gly Ser Ala Arg Lys Cys Ser Leu Thr Gly Lys Trp Thr Asn Asp Leu 385 390 395 400

Gly Ser Asn Met Thr Ile Gly Ala Val Asn Ser Arg Gly Glu Phe Thr 405 410 415

Gly Thr Tyr Ile Thr Ala Val Thr Ala Thr Ser Asn Glu Ile Lys Glu 420 425 430

Ser Pro Leu His Gly Thr Gln Asn Thr Ile Asn Lys Ser Gly Gly Ser 435 440 445

Thr Thr Val Phe Thr Gly Gln Cys Phe Ile Asp Arg Asn Gly Lys Glu 450 455 460

Val Leu Lys Thr Met Trp Leu Leu Arg Ser Ser Val Asn Asp Ile Gly 465 470 475 480

Asp Asp Trp Lys Ala Thr Arg Val Gly Ile Asn Ile Phe Thr Arg Leu 485 490 495

Arg Thr Gln Lys Glu Gly Gly Ser Gly Gly Ser Ala Arg Lys Cys Ser 500 505 510

Leu Thr Gly Lys Trp Thr Asn Asp Leu Gly Ser Asn Met Thr Ile Gly 515 520 525

Ala Val Asn Ser Arg Gly Glu Phe Thr Gly Thr Tyr Ile Thr Ala Val 530 535 540

Thr Ala Thr Ser Asn Glu Ile Lys Glu Ser Pro Leu His Gly Thr Gln 545 550 555 560

Asn Thr Ile Asn Lys Arg Thr Gln Pro Thr Phe Gly Phe Thr Val Asn 565 570 575

Trp Lys Phe Ser Glu 580

<210> 25

<211> 1746

<212> DNA

<213> Gallus gallus

<221> DNA

<223> DNA sequence which codes for scAvd of SEQ ID NO 24

<400> 25 atggtgcacg caacctcccc gctgctgctg ctgctgctgc tcagcctggc tctggtqqct 60 cccggcctct ctgccaggaa gaggacccag cccacctttg gcttcaccgt caattggaag 120 ttttcagagt ccaccactgt cttcacgggc cagtgcttca tagacaggaa tgggaaggag 180 gtcctgaaga ccatgtggct gctgcggtca agtgttaatg acattggtga tgactggaaa 240 gctaccaggg tcggcatcaa catcttcact cgcctgcgca cacagaagga gggaggctcc 300 ggaggeteeg ceagaaagtg etegetgaet gggaaatgga ceaacgatet gggeteeaac 360 atgaccatcg gggctgtgaa cagcagaggt gaattcacag gcacctacat cacagccqta 420 acagccacat caaatgagat caaagagtca ccactgcatg ggacacaaaa caccatcaac 480 aagtccggcg gatccaccac tgtcttcacg ggccagtgct tcatagacag gaatgggaag 540 gaggtcctga agaccatgtg gctgctgcgg tcaagtgtta atgacattgg tgatgactgg 600 aaagctacca gggtcggcat caacatcttc actcgcctgc gcacacagaa ggagggaggc 660 teeggagget eegecagaaa gtgetegetg aetgggaaat ggaccaacga tetgggetee 720 aacatgacca teggggetgt gaacagcaga ggtgaattca caggcaccta catcacagce 780 gtaacagcca catcaaatga gatcaaagag tcaccactgc atgggacaca aaacaccatc 840 aacaagagga cccagcccac ctttggcttc accgtcaatt ggaagttttc agagggaggt 900 teeggategg gateeggete tggeagegge aggacecage ceaeetttgg etteacegte 960

aattggaagt	tttcagagtc	caccactgtc	ttcacgggcc	agtgcttcat	agacaggaat	1020
gggaaggagg	tcctgaagac	catgtggctg	ctgcggtcaa	gtgttaatga	cattggtgat	1080
gactggaaag	ctaccagggt	cggcatcaac	atcttcactc	gcctgcgcac	acagaaggag	1140
ggaggctccg	gaggctccgc	cagaaagtgc	tcgctgactg	ggaaatggac	caacgatctg	1200
ggctccaaca	tgaccatcgg	ggctgtgaac	agcagaggtg	aattcacagg	cacctacatc	1260
acagccgtaa	cagccacatc	aaatgagatc	aaagagtcac	cactgcatgg	gacacaaaac	1320
accatcaaca	agtccggcgg	atccaccact	gtcttcacgg	gccagtgctt	catagacagg	1380
aatgggaagg	aggtcctgaa	gaccatgtgg	ctgctgcggt	caagtgttaa	tgacattggt	1440
gatgactgga	aagctaccag	ggtcggcatc	aacatcttca	ctcgcctgcg	cacacagaag	1500
gagggaggct	ccggaggctc	cgccagaaag	tgctcgctga	ctgggaaatg	gaccaacgat	1560
ctgggctcca	acatgaccat	cggggctgtg	aacagcagag	gtgaattcac	aggcacctac	1620
atcacagccg	taacagccac	atcaaatgag	atcaaagagt	caccactgca	tgggacacaa	1680
aacaccatca	acaagaggac	ccagcccacc	tttggcttca	ccgtcaattg	gaagttttca	1740
gagtga						1746

<210> 26

<211> 897

<212> DNA

<213> Gallus gallus

<221> DNA

<223> DNA sequence which codes for dcAvd of SEQ ID 2

<400> 26 atggtgcacg caacctcccc gctgctgctg ctgctgctgc tcagcctggc tctggtggct 60 cccggcctct ctgccaggaa gaggacccag cccacctttg gcttcaccgt caattggaag 120 ttttcagagt ccaccactgt cttcacgggc cagtgcttca tagacaggaa tgggaaggag 180 gtcctgaaga ccatgtggct gctgcggtca agtgttaatg acattggtga tgactggaaa 240 gctaccaggg tcggcatcaa catcttcact cgcctgcgca cacagaagga gggaggctcc 300 ggaggeteeg ecagaaagtg etegetgaet gggaaatgga ecaacgatet gggeteeaac 360 atgaccatcg gggctgtgaa cagcagaggt gaattcacag gcacctacat cacagccgta 420 acagccacat caaatgagat caaagagtca ccactgcatg ggacacaaaa caccatcaac 480 aagtccggcg gatccaccac tgtcttcacg ggccagtgct tcatagacag gaatgggaag 540 gaggtcctga agaccatgtg gctgctgcgg tcaagtgtta atgacattgg tgatgactgg 600 aaagctacca gggtcggcat caacatcttc actcgcctgc gcacacagaa ggagggaggc 660 tccggaggct ccgccagaaa gtgctcgctg actgggaaat ggaccaacga tctgggctcc 720 aacatgacca tcggggctgt gaacagcaga ggtgaattca caggcaccta catcacagcc 780 gtaacagcca catcaaatga gatcaaagag tcaccactgc atgggacaca aaacaccatc 840 aacaagagga cccagcccac ctttggcttc accgtcaatt ggaagttttc agagtga 897

<210> 27

<211> 31 <212> DNA <213> Artificial sequence

<223> primer cp34_C1

<400> 27

aatttaagct tatgttacgg ctgtgatgta g

31

<210> 28

<211> 290

<212> PRT

<213> Gallus gallus

<400> 28

Met Asn Lys Pro Ser Lys Phe Ala Leu Pro Leu Ala Phe Ala Ala Val

Thr Ala Ser Gly Val Ala Ser Ala Gly Thr Gln Pro Thr Phe Gly Phe 20 25

Thr Val Asn Trp Lys Phe Ser Glu Ser Thr Thr Val Phe Thr Gly Gln

Cys Phe Ile Asp Arg Asn Gly Lys Glu Val Leu Lys Thr Met Trp Leu

Leu Arg Ser Ser Val Asn Asp Ile Gly Asp Asp Trp Lys Ala Thr Arg 75

Val Gly Ile Asn Ile Phe Thr Arg Leu Arg Thr Gln Lys Glu Gly Gly 95

Ser Gly Gly Ser Ala Arg Lys Cys Ser Leu Thr Gly Lys Trp Thr Asn

Asp Leu Gly Ser Asn Met Thr Ile Gly Ala Val Asn Ser Arg Gly Glu 115 120

Phe Thr Gly Thr Tyr Ile Thr Ala Val Thr Ala Thr Ser Asn Glu Ile

140

12/13

135

Arg Thr Gln Pro Thr Phe Gly Phe Thr Val Asn Trp Lys Phe Ser Glu 180 185 190

Ser Thr Thr Val Phe Thr Gly Gln Cys Phe Ile Asp Arg Asn Gly Lys 195 200 205

Glu Val Leu Lys Thr Met Trp Leu Leu Arg Ser Ser Val Asn Asp Ile 210 215 220

Gly Asp Asp Trp Lys Ala Thr Arg Val Gly Ile Asn Ile Phe Thr Arg 225 230 235 240

Leu Arg Thr Gln Lys Glu Gly Gly Ser Gly Gly: Ser Ala Arg Lys Cys 245 250 255

Ser Leu Thr Gly Lys Trp Thr Asn Asp Leu Gly Ser Asn Met Thr Ile 260 265 270

Gly Ala Val Asn Ser Arg Gly Glu Phe Thr Gly Thr Tyr Ile Thr Ala 275 280 285

Val Thr 290

130

<210> 29 <211> 873 <212> DNA <213> Gallus gallus

<400> 29

atgaacaaac cctccaaatt cgctctgcg cttgccttcg ccgccgttac ggcctctggt 60
gttgcctcgg ctggtaccca gcccaccttt ggcttcaccg tcaattggaa gttttcagag 120
tccaccactg tcttcacggg ccagtgcttc atagacagga atgggaagga ggtcctgaag 180
accatgtggc tgctgcggtc aagtgttaat gacattggtg atgactggaa agctaccagg 240
gtcggcatca acatcttcac tcgcctgcgc acacagaagg agggaggctc cggaggctcc 300
gccagaaagt gctcgctgac tgggaaatgg accaacgatc tgggctccaa catgaccatc 360

ggggctgtga	acagcagagg	tgaattcaca	ggcacctaca	tcacagccgt	aacagccaca	420
tcaaatgaga	tcaaagagtc	accactgcat	gggacacaaa	acaccatcaa	caagtccggc	480
ggatccaaag	agtcaccact	gcatgggaca	caaaacacca	tcaacaagag	gacccagccc	540
acctttggct	tcaccgtcaa	ttggaagttt	tcagagtcca	ccactgtctt	cacgggccag	600
tgcttcatag	acaggaatgg	gaaggaggtc	ctgaagacca	tgtggctgct	gcggtcaagt	660
gttaatgaca	ttggtgatga	ctggaaagct	accagggtcg	gcatcaacat	cttcactcgc	720
ctgcgcacac	agaaggaggg	aggctccgga	ggctccgcca	gaaagtgctc	gctgactggg	780
aaatggacca	acgatctggg	ctccaacatg	accatcgggg	ctgtgaacag	cagaggtgaa	840
ttcacaggca	cctacatcac	agccgtaaca	taa			873